We claim:

1. A substantially purified nucleic acid molecule that encodes a maize or soybean gibberellin pathway enzyme or fragment thereof, wherein said maize or soybean gibberellin pathway enzyme is selected from the group consisting of:

(a) copalyl diphosphate synthase;

(b) *ent*-kaurene synthase;

(c) Dwarf3;

(d) gibberellin 20-oxidase;

(e) gibberellin 7-oxidase ;

(f) gibberellin 3 β-hydroxylase; and

(g) *ent*-kaurene oxidase.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 84.

3. A substantially purified maize or soybean gibberellin pathway enzyme or fragment thereof, wherein said maize or soybean gibberellin pathway enzyme is selected from the group consisting of

(a) copalyl diphosphate synthase or fragment thereof;

(b) *ent*-kaurene synthase or fragment thereof;

(c) Dwarf3 or fragment thereof;

(d) gibberellin 20-oxidase or fragment thereof;

(e) gibberellin 7-oxidase or fragment thereof;

(f) gibberellin 3 β-hydroxylase; and

(g) *ent*-kaurene oxidase.

4. A substantially purified maize or soybean gibberellin pathway enzyme or fragment thereof according to claim 3, wherein said maize or soybean gibberellin pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 84.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean gibberellin pathway enzyme or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a copalyl diphosphate synthase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a *ent*-kaurene synthase enzyme or fragment thereof;

(c) a nucleic acid sequence which encodes for a Dwarf3 enzyme or fragment thereof;

(d) a nucleic acid sequence which encodes for a gibberellin 20-oxidase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a gibberellin 7-oxidase enzyme or fragment thereof;

(f) a nucleic acid sequence which encodes for a gibberellin 3 β-hydroxylase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for an *ent*-kaurene oxidase; and

(h) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (g); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (g).

8. A method for determining a level or pattern in a plant cell of an gibberellin pathway enzyme in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 84 or compliments thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said gibberellin pathway enzyme;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said gibberellin pathway enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.